

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: NAKAMURA, SEIJI  
SAKURAI, TAKASHI  
NEZU, JUNI-ICHI
- (ii) TITLE OF INVENTION: GENE ENCODING ADSEVERIN
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
  - (B) STREET: P.O. Box 747
  - (C) CITY: Falls Church
  - (D) STATE: VA
  - (E) COUNTRY: USA
  - (F) ZIP: 22040-0747
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: MURPHY Jr., Gerald M.
  - (B) REGISTRATION NUMBER: 28,977
  - (C) REFERENCE/DOCKET NUMBER: 230-110P
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703) 205-8000
  - (B) TELEFAX: (703) 205-8050

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  

Lys	Val	Ala	His	Val	Lys	Gln	Ile	Pro	Phe	Asp	Ala
1				5						10	



(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Thr Asn Asp Leu Thr Ala Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ile Thr Asn Arg Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2418 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 27..2171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGCCGGAAC ATCGCGTGCC CGAGTC ATG GCC CAG GGG CTG TAC CAC GAG GAG 53  
Met Ala Gln Gly Leu Tyr His Glu Glu  
1 5

TTC GCC CGC GCG GGC AAG CGG GCG GGG CTG CAG GTC TGG AGA ATT GAG 101



Phe	Ala	Arg	Ala	Gly	Lys	Arg	Ala	Gly	Leu	Gln	Val	Trp	Arg	Ile	Glu			
10					15					20					25			
AAG	CTG	GAG	CTG	GTG	CCG	GTG	CCC	GAG	AGC	GCG	TAT	GGC	AAC	TTC	TAC			149
Lys	Leu	Glu	Leu	Val	Pro	Val	Pro	Glu	Ser	Ala	Tyr	Gly	Asn	Phe	Tyr			
				30				35						40				
GTC	GGG	GAT	GCC	TAC	CTG	GTG	CTC	CAC	ACG	ACG	CAG	GCC	AGC	CGG	GGC			197
Val	Gly	Asp	Ala	Tyr	Leu	Val	Leu	His	Thr	Thr	Gln	Ala	Ser	Arg	Gly			
			45					50					55					
TTC	ACC	TAC	CGC	CTG	CAC	TTC	TGG	CTG	GGA	AAG	GAG	TGT	ACT	CAG	GAT			245
Phe	Thr	Tyr	Arg	Leu	His	Phe	Trp	Leu	Gly	Lys	Glu	Cys	Thr	Gln	Asp			
		60					65				70							
GAA	AGC	ACA	GCA	GCT	GCC	ATC	TTT	ACT	GTT	CAG	ATG	GAT	GAC	TAT	TTG			293
Glu	Ser	Thr	Ala	Ala	Ala	Ile	Phe	Thr	Val	Gln	Met	Asp	Asp	Tyr	Leu			
	75					80				85								
GGT	GGC	AAA	CCT	GTG	CAG	AAC	AGA	GAA	CTT	CAA	GGC	TAT	GAG	TCT	ACG			341
Gly	Gly	Lys	Pro	Val	Gln	Asn	Arg	Glu	Leu	Gln	Gly	Tyr	Glu	Ser	Thr			
	90				95					100					105			
GAT	TTT	GTT	GGC	TAC	TTT	AAA	GGA	GGT	CTG	AAA	TAC	AAG	GCT	GGC	GGT			389
Asp	Phe	Val	Gly	Tyr	Phe	Lys	Gly	Gly	Leu	Lys	Tyr	Lys	Ala	Gly	Gly			
				110					115					120				
GTG	GCG	TCT	GGA	CTC	AAT	CAT	GTG	CTT	ACA	AAT	GAC	TTG	ACT	GCT	CAG			437
Val	Ala	Ser	Gly	Leu	Asn	His	Val	Leu	Thr	Asn	Asp	Leu	Thr	Ala	Gln			
			125					130					135					
AGG	CTC	CTG	CAT	GTG	AAA	GGT	CGG	AGA	GTC	GTC	AGG	GCC	ACG	GAA	GTT			485
Arg.	Leu	Leu	His	Val	Lys	Gly	Arg	Arg	Val	Val	Arg	Ala	Thr	Glu	Val			
		140					145					150						
CCC	CTA	AGC	TGG	GAC	AGT	TTC	AAC	AAG	GGT	GAC	TGC	TTC	ATC	ATT	GAC			533
Pro	Leu	Ser	Trp	Asp	Ser	Phe	Asn	Lys	Gly	Asp	Cys	Phe	Ile	Ile	Asp			
		155				160					165							
CTT	GGC	ACT	GAA	ATT	TAC	CAG	TGG	TGT	GGA	TCT	TCT	TGC	AAC	AAG	TAC			581
Leu	Gly	Thr	Glu	Ile	Tyr	Gln	Trp	Cys	Gly	Ser	Ser	Cys	Asn	Lys	Tyr			
	170				175					180					185			
GAG	CGC	CTG	AAG	GCC	AGC	CAG	GTT	GCC	ATC	GGC	ATT	CGG	GAC	AAT	GAA			629
Glu	Arg	Leu	Lys	Ala	Ser	Gln	Val	Ala	Ile	Gly	Ile	Arg	Asp	Asn	Glu			
				190					195					200				
AGG	AAA	GGC	AGA	GCT	CAG	CTG	ATT	GTG	GTA	GAA	GAA	GGG	AGT	GAA	CCA			677
Arg	Lys	Gly	Arg	Ala	Gln	Leu	Ile	Val	Val	Glu	Glu	Gly	Ser	Glu	Pro			
			205					210					215					
TCA	GAG	CTT	ACA	AAG	GTA	TTA	GGG	GAA	AAG	CCA	AAG	CTT	AGG	GAT	GGA			725
Ser	Glu	Leu	Thr	Lys	Val	Leu	Gly	Glu	Lys	Pro	Lys	Leu	Arg	Asp	Gly			
		220					225					230						
GAA	GAT	GAT	GAT	GAC	ATC	AAA	GCA	GAT	ATA	ACT	AAT	AGG	AAA	ATG	GCT			773
Glu	Asp	Asp	Asp	Asp	Ile	Lys	Ala	Asp	Ile	Thr	Asn	Arg	Lys	Met	Ala			
	235					240					245							
AAA	CTC	TAC	ATG	GTT	TCA	GAT	GCC	AGT	GGC	TCC	ATG	AAA	GTG	AGT	CTG			821
Lys	Leu	Tyr	Met	Val	Ser	Asp	Ala	Ser	Gly	Ser	Met	Lys	Val	Ser	Leu			



250	255	260	265	
GTG GCA GAA GAA AAC CCC TTC TCC ATG GCG ATG CTT CTG TCT GAA GAA Val Ala Glu Glu Asn Pro Phe Ser Met Ala Met Leu Leu Ser Glu Glu	270	275	280	869
TGC TTC ATT TTG GAC CAC GGT GCT GCA AAA CAG ATT TTT GTA TGG AAA Cys Phe Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe Val Trp Lys	285	290	295	917
GGT AAA GAT GCT AAT CCC CAG GAG AGA AAG GCT GCC ATG AAG ACA GCT Gly Lys Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met Lys Thr Ala	300	305	310	965
GAG GAA TTC CTA CAG CAA ATG AAT TAT TCT ACG AAT ACC CAA ATT CAA Glu Glu Phe Leu Gln Gln Met Asn Tyr Ser Thr Asn Thr Gln Ile Gln	315	320	325	1013
GTT CTT CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG TTC TTT AAG Val Leu Pro Glu Gly Gly Glu Thr Pro Ile Phe Lys Gln Phe Phe Lys	330	335	340	1061
GAC TGG AGA GAT AGA GAT CAG AGC GAT GGC TTC GGG AAA GTG TAT GTC Asp Trp Arg Asp Arg Asp Gln Ser Asp Gly Phe Gly Lys Val Tyr Val	350	355	360	1109
ACA GAA AAA GTG GCT CAC GTA AAA CAA ATT CCA TTT GAT GCC TCA AAA Thr Glu Lys Val Ala His Val Lys Gln Ile Pro Phe Asp Ala Ser Lys	365	370	375	1157
TTG CAC AGC TCC CCA CAA ATG GCA GCC CAG CAT CAC GTG GTG GAT GAC Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val Val Asp Asp	380	385	390	1205
GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA AAC AAC GGT AGG GTC Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu Asn Asn Gly Arg Val	395	400	405	1253
GAA ATT GAC CGA AAC TCG TAT GGT GAA TTC TAT GGT GGT GAT TGC TAC Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp Cys Tyr	410	415	420	1301
ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG ATT ATC TAC ACC TGG CAA Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr Trp Gln	430	435	440	1349
GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC TCC GCA TTC CTG ACT Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe Leu Thr	445	450	455	1397
GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG GCT GTG CAG ATT CGA GTC Val Gln Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln Ile Arg Val	460	465	470	1445
TCC CAA GGC AAA GAA CCT GCT CAC CTG CTG AGT TTG TTC AAA GAC AAA Ser Gln Gly Lys Glu Pro Ala His Leu Leu Ser Leu Phe Lys Asp Lys	475	480	485	1493
CCG CTC ATT ATT TAC AAG AAC GGA ACA TCA AAG AAA GAA GGT CAG GCA Pro Leu Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Glu Gly Gln Ala	490	495	500	1541



CCA GCC CCC CCT ATA CGC CTC TTT CAA GTC CGA AGA AAC CTG GCT TCG Pro Ala Pro Pro Ile Arg Leu Phe Gln Val Arg Arg Asn Leu Ala Ser 510 515 520	1589
ATC ACC AGA ATT ATG GAG GTA GAT GTT GAT GCA AAC TCA TTG AAT TCC Ile Thr Arg Ile Met Glu Val Asp Val Asp Ala Asn Ser Leu Asn Ser 525 530 535	1637
AAT GAT GTT TTT GTC CTG AAA CTG CGA CAA AAT AAT GGC TAC ATC TGG Asn Asp Val Phe Val Leu Lys Leu Arg Gln Asn Asn Gly Tyr Ile Trp 540 545 550	1685
ATA GGA AAA GGC TCC ACA CAG GAG GAG GAG AAA GGA GCA GAG TAC GTG Ile Gly Lys Gly Ser Thr Gln Glu Glu Glu Lys Gly Ala Glu Tyr Val 555 560 565	1733
GCA AGC GTC CTC AAA TGC AAA ACT TCG ACG ATT CAG GAA GGC AAG GAA Ala Ser Val Leu Lys Cys Lys Thr Ser Thr Ile Gln Glu Gly Lys Glu 570 575 580 585	1781
CCA GAG GAG TTT TGG AAT TCC CTT GGA GGG AAA AAA GAC TAC CAG ACC Pro Glu Glu Phe Trp Asn Ser Leu Gly Gly Lys Lys Asp Tyr Gln Thr 590 595 600	1829
TCT CCT CTG CTA GAA TCC CAG GCT GAA GAC CAT CCA CCT CGG CTT TAC Ser Pro Leu Leu Glu Ser Gln Ala Glu Asp His Pro Pro Arg Leu Tyr 605 610 615	1877
GGC TGC TCC AAC AAA ACT GGA AGA TTC ATT ATT GAA GAG GTT CCA GGA Gly Cys Ser Asn Lys Thr Gly Arg Phe Ile Ile Glu Glu Val Pro Gly 620 625 630	1925
GAG TTC ACC CAG GAT GAT TTA GCA GAA GAT GAT GTC ATG CTG TTA GAT Glu Phe Thr Gln Asp Asp Leu Ala Glu Asp Asp Val Met Leu Leu Asp 635 640 645	1973
GCT TGG GAA CAG ATT TTT ATT TGG ATT GGA AAA GAT GCC AAT GAA GTT Ala Trp Glu Gln Ile Phe Ile Trp Ile Gly Lys Asp Ala Asn Glu Val 650 655 660 665	2021
GAG AAA TCA GAA TCT CTG AAG TCT GCC AAA ATA TAC CTT GAG ACC GAC Glu Lys Ser Glu Ser Leu Lys Ser Ala Lys Ile Tyr Leu Glu Thr Asp 670 675 680	2069
CCT TCT GGA AGA GAC AAG AGG ACG CCA ATT GTC ATC ATA AAA CAG GGT Pro Ser Gly Arg Asp Lys Arg Thr Pro Ile Val Ile Ile Lys Gln Gly 685 690 695	2117
CAT GAG CCA CCT ACT TTC ACA GGC TGG TTC CTG GGC TGG GAT TCC AGC His Glu Pro Pro Thr Phe Thr Gly Trp Phe Leu Gly Trp Asp Ser Ser 700 705 710	2165
AGG TGG TAAACTGATT TTTGTAGGAA AAAACAAAT ATAATGGGGC AGCTGTCCCA Arg Trp 715	2221
GGGGGGAAGG AGGAGCTTGT TTAACTTTAG AAAATTAACC TCAGCCATAT GGCTATTTTT	2281
CCGTGCTTAG AATTGGTTTG AAATTTCTTT TAAACTGGAA TTTTCTTATG TTAATATTTT	2341



TATAACTTTT CTTATGGACC AATATTAGCT CTGCTGGATG CTGACATATC TTTATATATG 2401  
 ACTTTTAAAA GGGGCCG 2418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Gln Gly Leu Tyr His Glu Glu Phe Ala Arg Ala Gly Lys Arg  
 1 5 10 15  
 Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu Glu Leu Val Pro Val  
 20 25 30  
 Pro Glu Ser Ala Tyr Gly Asn Phe Tyr Val Gly Asp Ala Tyr Leu Val  
 35 40 45  
 Leu His Thr Thr Gln Ala Ser Arg Gly Phe Thr Tyr Arg Leu His Phe  
 50 55 60  
 Trp Leu Gly Lys Glu Cys Thr Gln Asp Glu Ser Thr Ala Ala Ala Ile  
 65 70 75 80  
 Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn  
 85 90 95  
 Arg Glu Leu Gln Gly Tyr Glu Ser Thr Asp Phe Val Gly Tyr Phe Lys  
 100 105 110  
 Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala Ser Gly Leu Asn His  
 115 120 125  
 Val Leu Thr Asn Asp Leu Thr Ala Gln Arg Leu Leu His Val Lys Gly  
 130 135 140  
 Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu Ser Trp Asp Ser Phe  
 145 150 155 160  
 Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln  
 165 170 175  
 Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg Leu Lys Ala Ser Gln  
 180 185 190  
 Val Ala Ile Gly Ile Arg Asp Asn Glu Arg Lys Gly Arg Ala Gln Leu  
 195 200 205  
 Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu Leu Thr Lys Val Leu  
 210 215 220  
 Gly Glu Lys Pro Lys Leu Arg Asp Gly Glu Asp Asp Asp Asp Ile Lys  
 225 230 235 240



Ala Asp Ile Thr Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp  
 245 250 255  
 Ala Ser Gly Ser Met Lys Val Ser Leu Val Ala Glu Glu Asn Pro Phe  
 260 265 270  
 Ser Met Ala Met Leu Leu Ser Glu Glu Cys Phe Ile Leu Asp His Gly  
 275 280 285  
 Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys Asp Ala Asn Pro Gln  
 290 295 300  
 Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu Phe Leu Gln Gln Met  
 305 310 315 320  
 Asn Tyr Ser Thr Asn Thr Gln Ile Gln Val Leu Pro Glu Gly Gly Glu  
 325 330 335  
 Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Arg Asp Arg Asp Gln  
 340 345 350  
 Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu Lys Val Ala His Val  
 355 360 365  
 Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His Ser Ser Pro Gln Met  
 370 375 380  
 Ala Ala Gln His His Val Val Asp Asp Gly Ser Gly Lys Val Gln Ile  
 385 390 395 400  
 Trp Arg Val Glu Asn Asn Gly Arg Val Glu Ile Asp Arg Asn Ser Tyr  
 405 410 415  
 Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro  
 420 425 430  
 Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala Asn Ala Thr Arg Asp  
 435 440 445  
 Glu Leu Thr Thr Ser Ala Phe Leu Thr Val Gln Leu Asp Arg Ser Leu  
 450 455 460  
 Gly Gly Gln Ala Val Gln Ile Arg Val Ser Gln Gly Lys Glu Pro Ala  
 465 470 475 480  
 His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu Ile Ile Tyr Lys Asn  
 485 490 495  
 Gly Thr Ser Lys Lys Glu Gly Gln Ala Pro Ala Pro Pro Ile Arg Leu  
 500 505 510  
 Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr Arg Ile Met Glu Val  
 515 520 525  
 Asp Val Asp Ala Asn Ser Leu Asn Ser Asn Asp Val Phe Val Leu Lys  
 530 535 540  
 Leu Arg Gln Asn Asn Gly Tyr Ile Trp Ile Gly Lys Gly Ser Thr Gln  
 545 550 555 560  
 Glu Glu Glu Lys Gly Ala Glu Tyr Val Ala Ser Val Leu Lys Cys Lys



	565		570		575
Thr Ser Thr	Ile Gln Glu Gly Lys Glu Pro Glu Glu Phe Trp Asn Ser				
	580		585		590
Leu Gly Gly	Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Ser Gln				
	595		600		605
Ala Glu Asp	His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly				
	610		615		620
Arg Phe Ile	Ile Glu Glu Val Pro Gly Glu Phe Thr Gln Asp Asp Leu				
	625		630		635
Ala Glu Asp	Asp Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile				
	645		650		655
Trp Ile Gly	Lys Asp Ala Asn Glu Val Glu Lys Ser Glu Ser Leu Lys				
	660		665		670
Ser Ala Lys	Ile Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg				
	675		680		685
Thr Pro Ile	Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr				
	690		695		700
Gly Trp Phe	Leu Gly Trp Asp Ser Ser Arg Trp				
	705		710		715

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 79..2223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGGTTCTCTC CTGCTGCTCT CGGTTTAGTC CAAGATCAGC GATATCACGC GTCCCCCGGA	60
GCATCGCGTG CAGGAGCC ATG GCG CGG GAG CTA TAC CAC GAA GAG TTC GCC	111
Met Ala Arg Glu Leu Tyr His Glu Glu Phe Ala	
1 5 10	
CGG GCG GGC AAG CAG GCG GGG CTG CAG GTC TGG AGG ATT GAG AAG CTG	159
Arg Ala Gly Lys Gln Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu	
15 20 25	
GAG CTG GTG CCC GTG CCC CAG AGC GCT CAC GGC GAC TTC TAC GTC GGG	207
Glu Leu Val Pro Val Pro Gln Ser Ala His Gly Asp Phe Tyr Val Gly	
30 35 40	



GAT GCC TAC CTG GTG CTG CAC ACG GCC AAG ACG AGC CGA GGC TTC ACC Asp Ala Tyr Leu Val Leu His Thr Ala Lys Thr Ser Arg Gly Phe Thr 45 50 55	255
TAC CAC CTG CAC TTC TGG CTC GGA AAG GAG TGT TCC CAG GAT GAA AGC Tyr His Leu His Phe Trp Leu Gly Lys Glu Cys Ser Gln Asp Glu Ser 60 65 70 75	303
ACA GCT GCT GCC ATC TTC ACT GTT CAG ATG GAT GAC TAT TTG GGT GGC Thr Ala Ala Ala Ile Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly 80 85 90	351
AAG CCA GTG CAG AAT AGA GAA CTT CAA GGA TAT GAG TCT AAT GAC TTT Lys Pro Val Gln Asn Arg Glu Leu Gln Gly Tyr Glu Ser Asn Asp Phe 95 100 105	399
GTT AGC TAT TTC AAA GGC GGT CTG AAA TAC AAG GCT GGA GGC GTG GCA Val Ser Tyr Phe Lys Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala 110 115 120	447
TCT GGA TTA AAT CAT GTT CTT ACG AAC GAC CTG ACA GCC AAG AGG CTC Ser Gly Leu Asn His Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu 125 130 135	495
CTA CAT GTG AAG GGT CGT AGA GTG GTG AGA GCC ACA GAA GTT CCC CTT Leu His Val Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu 140 145 150 155	543
AGC TGG GAC AGT TTC AAC AAG GGT GAC TGC TTC ATC ATT GAC CTT GGC Ser Trp Asp Ser Phe Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly 160 165 170	591
ACC GAA ATT TAT CAG TGG TGT GGT TCC TCG TGC AAC AAA TAT GAA CGT Thr Glu Ile Tyr Gln Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg 175 180 185	639
CTG AAG GCA AAC CAG GTA GCT ACT GGC ATT CGG TAC AAT GAA AGG AAA Leu Lys Ala Asn Gln Val Ala Thr Gly Ile Arg Tyr Asn Glu Arg Lys 190 195 200	687
GGA AGG TCT GAA CTA ATT GTC GTG GAA GAA GGA AGT GAA CCC TCA GAA Gly Arg Ser Glu Leu Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu 205 210 215	735
CTT ATA AAG GTC TTA GGG GAA AAG CCA GAG CTT CCA GAT GGA GGT GAT Leu Ile Lys Val Leu Gly Glu Lys Pro Glu Leu Pro Asp Gly Gly Asp 220 225 230 235	783
GAT GAT GAC ATT ATA GCA GAC ATA AGT AAC AGG AAA ATG GCT AAA CTA Asp Asp Asp Ile Ile Ala Asp Ile Ser Asn Arg Lys Met Ala Lys Leu 240 245 250	831
TAC ATG GTT TCA GAT GCA AGT GGC TCC ATG AGA GTG ACT GTG GTG GCA Tyr Met Val Ser Asp Ala Ser Gly Ser Met Arg Val Thr Val Val Ala 255 260 265	879
GAA GAA AAC CCC TTC TCA ATG GCA ATG CTG CTG TCT GAA GAA TGC TTT Glu Glu Asn Pro Phe Ser Met Ala Met Leu Leu Ser Glu Glu Cys Phe 270 275 280	927



ATT TTG GAC CAC GGG GCT GCC AAA CAA ATT TTC GTA TGG AAA GGT AAA Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys 285 290 295	975
GAT GCT AAT CCC CAA GAG AGG AAG GCT GCA ATG AAG ACA GCT GAA GAA Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu 300 305 310 315	1023
TTT CTA CAG CAA ATG AAT TAT TCC AAG AAT ACC CAA ATT CAA GTT CTT Phe Leu Gln Gln Met Asn Tyr Ser Lys Asn Thr Gln Ile Gln Val Leu 320 325 330	1071
CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG TTT TTT AAG GAC TGG Pro Glu Gly Gly Glu Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp 335 340 345	1119
AGA GAT AAA GAT CAG AGT GAT GGC TTC GGG AAA GTT TAT GTC ACA GAG Arg Asp Lys Asp Gln Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu 350 355 360	1167
AAA GTG GCT CAA ATA AAA CAA ATT CCC TTT GAT GCC TCA AAA TTA CAC Lys Val Ala Gln Ile Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His 365 370 375	1215
AGT TCT CCG CAG ATG GCA GCC CAG CAC AAT ATG GTG GAT GAT GGT TCT Ser Ser Pro Gln Met Ala Ala Gln His Asn Met Val Asp Asp Gly Ser 380 385 390 395	1263
GGC AAA GTG GAG ATT TGG CGT GTA GAA AAC AAT GGT AGG ATC CAA GTT Gly Lys Val Glu Ile Trp Arg Val Glu Asn Asn Gly Arg Ile Gln Val 400 405 410	1311
GAC CAA AAC TCA TAT GGT GAA TTC TAT GGT GGT GAC TGC TAC ATC ATA Asp Gln Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile 415 420 425	1359
CTC TAC ACC TAT CCC AGA GGA CAG ATT ATC TAC ACG TGG CAA GGA GCA Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala 430 435 440	1407
AAT GCC ACA CGA GAT GAG CTG ACA ACA TCT GCG TTC CTG ACT GTT CAG Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe Leu Thr Val Gln 445 450 455	1455
TTG GAT CGG TCC CTT GGA GGA CAG GCT GTG CAG ATC CGA GTC TCC CAA Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln Ile Arg Val Ser Gln 460 465 470 475	1503
GGC AAA GAG CCT GTT CAC CTA CTG AGT TTG TTC AAA GAC AAA CCG CTC Gly Lys Glu Pro Val His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu 480 485 490	1551
ATT ATT TAC AAG AAT GGA ACA TCA AAG AAA GGA GGT CAG GCA CCT GCT Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Gly Gly Gln Ala Pro Ala 495 500 505	1599
CCC CCT ACA CGC CTC TTT CAA GTC CGG AGA AAC CTG GCA TCT ATC ACC Pro Pro Thr Arg Leu Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr 510 515 520	1647
AGA ATT GTG GAG GTT GAT GTT GAT GCA AAT TCA CTG AAT TCT AAC GAT	1695



Arg	Ile	Val	Glu	Val	Asp	Val	Asp	Ala	Asn	Ser	Leu	Asn	Ser	Asn	Asp		
525						530					535						
GTT	TGT	GTC	CTG	AAA	CTG	CCA	CAA	AAT	AGT	GGC	TAC	ATC	TGG	GTA	GGA	1743	
Val	Cys	Val	Leu	Lys	Leu	Pro	Gln	Asn	Ser	Gly	Tyr	Ile	Trp	Val	Gly		
540					545					550					555		
AAA	GGT	GCT	AGC	CAG	GAG	GAG	GAG	AAA	GGA	GCA	GAG	TAT	GTA	GCA	AGT	1791	
Lys	Gly	Ala	Ser	Gln	Glu	Glu	Glu	Lys	Gly	Ala	Glu	Tyr	Val	Ala	Ser		
				560					565					570			
GTC	CTA	AAG	TGC	AAA	ACC	TTA	AGG	ATC	CAA	GAA	GGC	GAG	GAG	CCA	GAG	1839	
Val	Leu	Lys	Cys	Lys	Thr	Leu	Arg	Ile	Gln	Glu	Gly	Glu	Glu	Pro	Glu		
			575					580						585			
GAG	TTC	TGG	AAT	TCC	CTT	GGA	GGG	AAA	AAA	GAC	TAC	CAG	ACC	TCA	CCA	1887	
Glu	Phe	Trp	Asn	Ser	Leu	Gly	Gly	Lys	Lys	Asp	Tyr	Gln	Thr	Ser	Pro		
		590					595					600					
CTA	CTG	GAA	ACC	CAG	GCT	GAA	GAC	CAT	CCA	CCT	CGG	CTT	TAC	GGC	TGC	1935	
Leu	Leu	Glu	Thr	Gln	Ala	Glu	Asp	His	Pro	Pro	Arg	Leu	Tyr	Gly	Cys		
		605				610					615						
TCT	AAC	AAA	ACT	GGA	AGA	TTT	GTT	ATT	GAA	GAG	ATT	CCA	GGA	GAG	TTC	1983	
Ser	Asn	Lys	Thr	Gly	Arg	Phe	Val	Ile	Glu	Glu	Ile	Pro	Gly	Glu	Phe		
		620			625					630					635		
ACC	CAG	GAT	GAT	TTA	GCT	GAA	GAT	GAT	GTC	ATG	TTA	CTA	GAT	GCT	TGG	2031	
Thr	Gln	Asp	Asp	Leu	Ala	Glu	Asp	Asp	Val	Met	Leu	Leu	Asp	Ala	Trp		
				640					645					650			
GAA	CAG	ATA	TTT	ATT	TGG	ATT	GGC	AAA	GAT	GCT	AAT	GAA	GTT	GAG	AAA	2079	
Glu	Gln	Ile	Phe	Ile	Trp	Ile	Gly	Lys	Asp	Ala	Asn	Glu	Val	Glu	Lys		
			655					660					665				
AAA	GAA	TCT	CTG	AAG	TCT	GCC	AAA	ATG	TAC	CTT	GAG	ACA	GAC	CCT	TCT	2127	
Lys	Glu	Ser	Leu	Lys	Ser	Ala	Lys	Met	Tyr	Leu	Glu	Thr	Asp	Pro	Ser		
		670					675					680					
GGA	AGA	GAC	AAG	AGG	ACA	CCA	ATT	GTC	ATC	ATA	AAA	CAG	GGC	CAT	GAG	2175	
Gly	Arg	Asp	Lys	Arg	Thr	Pro	Ile	Val	Ile	Ile	Lys	Gln	Gly	His	Glu		
		685				690					695						
CCA	CCC	ACA	TTC	ACA	GGC	TGG	TTC	CTG	GGC	TGG	GAT	TCC	AGC	AAG	TGG	2223	
Pro	Pro	Thr	Phe	Thr	Gly	Trp	Phe	Leu	Gly	Trp	Asp	Ser	Ser	Lys	Trp		
					705					710					715		
TAAATTGGTA	TTTGTA	AAAAA	GCAAACAAAC	ATTACAAGGC	AGTTATCTCA	TTGCTGTTTT										2283	
GGGAGAGGAA	CGGGAAAAAGC	TTTTTGCTTA	TTTGTCTTTT	GAAAATTAAG	GCTGGGCGCG											2343	
GTGGCTCACA	CCTGTAATCC	CAGCACTTTG	AGAGGATGAG	GTAGGCGGAT	CACTGGGGTTC											2403	
AGGATTTCTGA	GACCAGCCTG	GCCAACATGG	CGAAACCTCG	CCTCTACTAA	AAATACAAAA											2463	
AAATTAGCTG	CGCGTGCTGG	TGCACGCCTG	TAGTCCCTGC	TACTTGGAAG	GCTGAGACAG											2523	
GAAAAATTGCT	TGAGCCCAGG	AGGCTGAGGT	TGCAGTGAGC	CAGGATTGCG	CCACCACACT											2583	
CCAGCCTGGG	CAACAGAGAC	TCTGTCTCAA	AAAAAAAAAA	AAAAAAA												2630	



(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Arg Glu Leu Tyr His Glu Glu Phe Ala Arg Ala Gly Lys Gln  
1 5 10 15  
Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu Glu Leu Val Pro Val  
20 25 30  
Pro Gln Ser Ala His Gly Asp Phe Tyr Val Gly Asp Ala Tyr Leu Val  
35 40 45  
Leu His Thr Ala Lys Thr Ser Arg Gly Phe Thr Tyr His Leu His Phe  
50 55 60  
Trp Leu Gly Lys Glu Cys Ser Gln Asp Glu Ser Thr Ala Ala Ala Ile  
65 70 75 80  
Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn  
85 90 95  
Arg Glu Leu Gln Gly Tyr Glu Ser Asn Asp Phe Val Ser Tyr Phe Lys  
100 105 110  
Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala Ser Gly Leu Asn His  
115 120 125  
Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu Leu His Val Lys Gly  
130 135 140  
Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu Ser Trp Asp Ser Phe  
145 150 155 160  
Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln  
165 170 175  
Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg Leu Lys Ala Asn Gln  
180 185 190  
Val Ala Thr Gly Ile Arg Tyr Asn Glu Arg Lys Gly Arg Ser Glu Leu  
195 200 205  
Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu Leu Ile Lys Val Leu  
210 215 220  
Gly Glu Lys Pro Glu Leu Pro Asp Gly Gly Asp Asp Asp Asp Ile Ile  
225 230 235 240  
Ala Asp Ile Ser Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp  
245 250 255  
Ala Ser Gly Ser Met Arg Val Thr Val Val Ala Glu Glu Asn Pro Phe



260										265										270															
Ser	Met	Ala	Met	Leu	Leu	Ser	Glu	Glu	Cys	Phe	Ile	Leu	Asp	His	Gly																				
		275					280					285																							
Ala	Ala	Lys	Gln	Ile	Phe	Val	Trp	Lys	Gly	Lys	Asp	Ala	Asn	Pro	Gln																				
		290				295					300																								
Glu	Arg	Lys	Ala	Ala	Met	Lys	Thr	Ala	Glu	Glu	Phe	Leu	Gln	Gln	Met																				
305					310					315					320																				
Asn	Tyr	Ser	Lys	Asn	Thr	Gln	Ile	Gln	Val	Leu	Pro	Glu	Gly	Gly	Glu																				
				325				330							335																				
Thr	Pro	Ile	Phe	Lys	Gln	Phe	Phe	Lys	Asp	Trp	Arg	Asp	Lys	Asp	Gln																				
			340					345						350																					
Ser	Asp	Gly	Phe	Gly	Lys	Val	Tyr	Val	Thr	Glu	Lys	Val	Ala	Gln	Ile																				
		355					360					365																							
Lys	Gln	Ile	Pro	Phe	Asp	Ala	Ser	Lys	Leu	His	Ser	Ser	Pro	Gln	Met																				
		370				375					380																								
Ala	Ala	Gln	His	Asn	Met	Val	Asp	Asp	Gly	Ser	Gly	Lys	Val	Glu	Ile																				
385					390					395					400																				
Trp	Arg	Val	Glu	Asn	Asn	Gly	Arg	Ile	Gln	Val	Asp	Gln	Asn	Ser	Tyr																				
				405					410					415																					
Gly	Glu	Phe	Tyr	Gly	Gly	Asp	Cys	Tyr	Ile	Ile	Leu	Tyr	Thr	Tyr	Pro																				
			420				425						430																						
Arg	Gly	Gln	Ile	Ile	Tyr	Thr	Trp	Gln	Gly	Ala	Asn	Ala	Thr	Arg	Asp																				
		435					440					445																							
Glu	Leu	Thr	Thr	Ser	Ala	Phe	Leu	Thr	Val	Gln	Leu	Asp	Arg	Ser	Leu																				
		450				455					460																								
Gly	Gly	Gln	Ala	Val	Gln	Ile	Arg	Val	Ser	Gln	Gly	Lys	Glu	Pro	Val																				
465					470					475					480																				
His	Leu	Leu	Ser	Leu	Phe	Lys	Asp	Lys	Pro	Leu	Ile	Ile	Tyr	Lys	Asn																				
				485					490				495																						
Gly	Thr	Ser	Lys	Lys	Gly	Gly	Gln	Ala	Pro	Ala	Pro	Pro	Thr	Arg	Leu																				
			500					505					510																						
Phe	Gln	Val	Arg	Arg	Asn	Leu	Ala	Ser	Ile	Thr	Arg	Ile	Val	Glu	Val																				
		515					520					525																							
Asp	Val	Asp	Ala	Asn	Ser	Leu	Asn	Ser	Asn	Asp	Val	Cys	Val	Leu	Lys																				
		530				535					540																								
Leu	Pro	Gln	Asn	Ser	Gly	Tyr	Ile	Trp	Val	Gly	Lys	Gly	Ala	Ser	Gln																				
545					550					555					560																				
Glu	Glu	Glu	Lys	Gly	Ala	Glu	Tyr	Val	Ala	Ser	Val	Leu	Lys	Cys	Lys																				
				565					570					575																					
Thr	Leu	Arg	Ile	Gln	Glu	Gly	Glu	Glu	Pro	Glu	Glu	Phe	Trp	Asn	Ser																				
			580				585						590																						



Leu Gly Gly Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Thr Gln  
 595 600 605  
 Ala Glu Asp His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly  
 610 615 620  
 Arg Phe Val Ile Glu Glu Ile Pro Gly Glu Phe Thr Gln Asp Asp Leu  
 625 630 635 640  
 Ala Glu Asp Asp Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile  
 645 650 655  
 Trp Ile Gly Lys Asp Ala Asn Glu Val Glu Lys Lys Glu Ser Leu Lys  
 660 665 670  
 Ser Ala Lys Met Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg  
 675 680 685  
 Thr Pro Ile Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr  
 690 695 700  
 Gly Trp Phe Leu Gly Trp Asp Ser Ser Lys Trp  
 705 710 715

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Asn His Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu Leu His  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Val Tyr Val Thr Glu Lys Val Ala Gln Ile Lys Gln Ile Pro Phe



1

5

10

15

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 782 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu  
 1 5 10 15

Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg  
 20 25 30

Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg  
 35 40 45

Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys  
 50 55 60

Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro  
 65 70 75 80

Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val  
 85 90 95

Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu  
 100 105 110

His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala  
 115 120 125

Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val  
 130 135 140

Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr  
 145 150 155 160

Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe  
 165 170 175

Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val  
 180 185 190

Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu  
 195 200 205

Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile  
 210 215 220

His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala  
 225 230 235 240



Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala  
 245 250 255  
 Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln  
 260 265 270  
 Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala  
 275 280 285  
 Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser  
 290 295 300  
 Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro  
 305 310 315 320  
 Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His  
 325 330 335  
 Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr  
 340 345 350  
 Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys  
 355 360 365  
 Met Asp Tyr Pro Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly  
 370 375 380  
 Glu Thr Pro Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp  
 385 390 395 400  
 Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn  
 405 410 415  
 Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala  
 420 425 430  
 Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln  
 435 440 445  
 Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr  
 450 455 460  
 Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr  
 465 470 475 480  
 Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala  
 485 490 495  
 Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln  
 500 505 510  
 Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln  
 515 520 525  
 Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met  
 530 535 540  
 Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro  
 545 550 555 560



Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr  
 565 570 575  
 Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp  
 580 585 590  
 Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr  
 595 600 605  
 Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val  
 610 615 620  
 Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly  
 625 630 635 640  
 Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg  
 645 650 655  
 Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys  
 660 665 670  
 Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu  
 675 680 685  
 Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp  
 690 695 700  
 Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys  
 705 710 715 720  
 Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala  
 725 730 735  
 Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu  
 740 745 750  
 Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp  
 755 760 765  
 Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala  
 770 775 780

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Thr Lys Leu Ser Ala Gln Val Lys Gly Ser Leu Asn Ile Thr Thr  
 1 5 10 15  
 Pro Gly Leu Gln Ile Trp Arg Ile Glu Ala Met Gln Met Val Pro Val



[illegible]



Asn Arg Thr Ser Gly Leu Gly Lys Thr His Thr Val Gly Ser Val Ala  
 355 360 365  
 Lys Val Glu Gln Val Lys Phe Asp Ala Thr Ser Met His Val Lys Pro  
 370 375 380  
 Gln Val Ala Ala Gln Gln Lys Met Val Asp Asp Gly Ser Gly Glu Val  
 385 390 395 400  
 Gln Val Trp Arg Ile Glu Asn Leu Glu Leu Val Pro Val Asp Ser Lys  
 405 410 415  
 Trp Leu Gly His Phe Tyr Gly Gly Asp Cys Tyr Leu Leu Leu Tyr Thr  
 420 425 430  
 Tyr Leu Ile Gly Glu Lys Gln His Tyr Leu Leu Tyr Val Trp Gln Gly  
 435 440 445  
 Ser Gln Ala Ser Gln Asp Glu Ile Thr Ala Ser Ala Tyr Gln Ala Val  
 450 455 460  
 Ile Leu Asp Gln Lys Tyr Asn Gly Glu Pro Val Gln Ile Arg Val Pro  
 465 470 475 480  
 Met Gly Lys Glu Pro Pro His Leu Met Ser Ile Phe Lys Gly Arg Met  
 485 490 495  
 Val Val Tyr Gln Gly Gly Thr Ser Arg Thr Asn Asn Leu Glu Thr Gly  
 500 505 510  
 Pro Ser Thr Arg Leu Phe Gln Val Gln Gly Thr Gly Ala Asn Asn Thr  
 515 520 525  
 Lys Ala Phe Glu Val Pro Ala Arg Ala Asn Phe Leu Asn Ser Asn Asp  
 530 535 540  
 Val Phe Val Leu Lys Thr Gln Ser Cys Cys Tyr Leu Trp Cys Gly Lys  
 545 550 555 560  
 Gly Cys Ser Gly Asp Glu Arg Glu Met Ala Lys Met Val Ala Asp Thr  
 565 570 575  
 Ile Ser Arg Thr Glu Lys Gln Val Val Val Glu Gly Gln Glu Pro Ala  
 580 585 590  
 Asn Phe Trp Met Ala Leu Gly Gly Lys Ala Pro Tyr Ala Asn Thr Lys  
 595 600 605  
 Arg Leu Gln Glu Glu Asn Leu Val Ile Thr Pro Arg Leu Phe Glu Cys  
 610 615 620  
 Ser Asn Lys Thr Gly Arg Phe Leu Ala Thr Glu Ile Pro Asp Phe Asn  
 625 630 635 640  
 Gln Asp Asp Leu Glu Glu Asp Asp Val Phe Leu Leu Asp Val Trp Asp  
 645 650 655  
 Gln Val Phe Phe Trp Ile Gly Lys His Ala Asn Glu Glu Glu Lys Lys  
 660 665 670



Ala	Ala	Ala	Thr	Thr	Ala	Gln	Glu	Tyr	Leu	Lys	Thr	His	Pro	Ser	Gly	
		675					680					685				
Arg	Asp	Pro	Glu	Thr	Pro	Ile	Ile	Val	Val	Lys	Gln	Gly	His	Glu	Pro	
	690					695					700					
Pro	Thr	Phe	Thr	Gly	Trp	Phe	Leu	Ala	Trp	Asp	Pro	Phe	Lys	Trp	Ser	
705					710					715					720	
Asn	Thr	Lys	Ser	Tyr	Glu	Asp	Leu	Lys	Ala	Glu	Ser	Gly	Asn	Leu	Arg	
				725					730					735		
Asp	Trp	Ser	Gln	Ile	Thr	Ala	Glu	Val	Thr	Ser	Pro	Lys	Val	Asp	Val	
			740					745					750			
Phe	Asn	Ala	Asn	Ser	Asn	Leu	Ser	Ser	Gly	Pro	Leu	Pro	Ile	Phe	Pro	
		755				760						765				
Leu	Glu	Gln	Leu	Val	Asn	Lys	Pro	Val	Glu	Glu	Leu	Pro	Glu	Gly	Val	
	770					775					780					
Asp	Pro	Ser	Arg	Lys	Glu	Glu	His	Leu	Ser	Ile	Glu	Asp	Phe	Thr	Gln	
785					790					795					800	
Ala	Phe	Gly	Met	Thr	Pro	Ala	Ala	Phe	Ser	Ala	Leu	Pro	Arg	Trp	Lys	
				805					810					815		
Gln	Gln	Asn	Leu	Lys	Lys	Glu	Lys	Gly	Leu	Phe						
			820					825								

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATGCGGATC CAAYGAYYTN ACNGCNCA

28

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATGCATCGA TACRTGNGCN ACYTTYTC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCGAGGGTG GCGACGACTC C

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGGCCGCTT GACACCAGAC CAA

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:



CAGCTATGAC CATGATTACG CCAA

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGACGGCCA GTGAATTGCG TAAT

24

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys	Val	Ala	Lys	Val	Glu	Gln	Val	Lys	Phe	Asp	Ala
1			5					10			